

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,132

DATE: 12/12/2001

TIME: 14:26:53

Input Set : A:\00-62.txt

Output Set: N:\CRF3\12112001\I003132.raw

ENTERED

4 <110> APPLICANT: Fox, Brian A.
5 Gao, Zeren
6 Shoemaker, Kimberly E.
8 <120> TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5
10 <130> FILE REFERENCE: 00-62
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/003,132
C--> 12 <141> CURRENT FILING DATE: 2001-11-15
12 <150> PRIOR APPLICATION NUMBER: US 60/249,004
13 <151> PRIOR FILING DATE: 2000-11-15
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3151
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (76)...(2223)
28 <400> SEQUENCE: 1

29	gcccggcccg ggcagctgcg gctcgggata cgctcagggg aggccgagct tgccaagctg	60
30	gcgcccagcg gggtc atg gtg ccc ggc gcc cgc ggc ggc ggc gca ctg gcg	111
31	Met Val Pro Gly Ala Arg Gly Gly Gly Ala Leu Ala	
32	1 5 10	
34	cgg gct gcc ggg cgg ggc ctc ctg gct ttg ctg ctc gcg gtc tcc gcc	159
35	Arg Ala Ala Gly Arg Gly Leu Leu Ala Leu Leu Ala Val Ser Ala	
36	15 20 25	
38	ccg ctc cgg ctg cag gcg gag gag ctg ggt gat ggc tgt gga cac cta	207
39	Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu	
40	30 35 40	
43	gtg act tat cag gat agt ggc aca atg aca tct aag aat tat ccc ggg	255
44	Val Thr Tyr Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly	
45	45 50 55 60	
47	acc tac ccc aat cac act gtt tgc gaa aag aca att aca gta cca aag	303
48	Thr Tyr Pro Asn His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys	
49	65 70 75	
51	ggg aaa aga ctg att ctg agg ttg gga gat ttg gat atc gaa tcc cag	351
52	Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln	
53	80 85 90	
55	acc tgt gct tct gac tat ctt ctc ttc acc agc tct tca gat caa tat	399
56	Thr Cys Ala Ser Asp Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr	
57	95 100 105	
59	ggt cca tac tgt gga agt atg act gtt ccc aaa gaa ctc ttg ttg aac	447
60	Gly Pro Tyr Cys Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn	
61	110 115 120	
63	aca agt gaa gta acc gtc cgc ttt gag agt gga tcc cac att tct ggc	495
64	Thr Ser Glu Val Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly	
65	125 130 135 140	

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67	cgg ggt ttt ttg ctg acc tat gcg agc agc gac cat cca gat tta ata	543
68	Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile	
69	145 150 155	
71	aca tgt ttg gaa cga gct agc cat tat ttg aag aca gaa tac agc aaa	591
72	Thr Cys Leu Glu Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys	
73	160 165 170	
75	ttc tgc cca gct ggt tgt aga gac gta gca gga gac att tct ggg aat	639
76	Phe Cys Pro Ala Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn	
77	175 180 185	
79	atg gta gat gga tat aga gat acc tct tta ttg tgc aaa gct gcc atc	687
80	Met Val Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile	
81	190 195 200	
83	cat gca gga ata att gct gat gaa cta ggt ggc cag atc agt gtg ctt	735
84	His Ala Gly Ile Ile Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu	
85	205 210 215 220	
87	cag cgc aaa ggg atc agt cga tat gaa ggg att ctg gcc aat ggt gtt	783
88	Gln Arg Lys Gly Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val	
89	225 230 235	
91	ctt tcg agg gat ggt tcc ctg tca gac aag cga ttt ctg ttt acc tcc	831
92	Leu Ser Arg Asp Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser	
93	240 245 250	
95	aat ggt tgc agc aga tcc ttg agt ttt gaa cct gac ggg caa atc aga	879
96	Asn Gly Cys Ser Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg	
97	255 260 265	
99	gct tct tcc tca tgg cag tcg gtc aat gag agt gga gac caa gtt cac	927
100	Ala Ser Ser Ser Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His	
101	270 275 280	
103	tgg tct cct ggc caa gcc cga ctt cag gac caa ggc cca tca tgg gct	975
104	Trp Ser Pro Gly Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala	
105	285 290 295 300	
107	tcg ggc gac agt agc aac aac cac aaa cca gag tgg ctg gag atc	1023
108	Ser Gly Asp Ser Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile	
109	305 310 315	
111	gat ttg ggg gag aaa aag aaa ata aca gga att agg acc aca gga tct	1071
112	Asp Leu Gly Glu Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser	
113	320 325 330	
115	aca cag tcg aac ttc aac ttt tat gtt aag agt ttt gtg atg aac ttc	1119
116	Thr Gln Ser Asn Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe	
117	335 340 345	
119	aaa aac aat aat tct aag tgg aag acc tat aaa gga att gtg aat aat	1167
120	Lys Asn Asn Asn Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn	
121	350 355 360	
123	gaa gaa aag gtg ttt cag ggt aac tct aac ttt cgg gac cca gtg caa	1215
124	Glu Glu Lys Val Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln	
125	365 370 375 380	
128	aac aat ttc atc cct ccc atc gtg gcc aga tat gtg cgg gtt gtc ccc	1263
129	Asn Asn Phe Ile Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro	
130	385 390 395	
132	cag aca tgg cac cag agg ata gcc ttg aag gtg gag ctc att ggt tgc	1311

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133	Gln	Thr	Trp	His	Gln	Arg	Ile	Ala	Leu	Lys	Val	Glu	Leu	Ile	Gly	Cys	
134				400					405					410			
136	cag	att	aca	caa	ggt	aat	gat	tca	ttg	gtg	tgg	cgc	aag	aca	agt	caa	1359
137	Gln	Ile	Thr	Gln	Gly	Asn	Asp	Ser	Leu	Val	Trp	Arg	Lys	Thr	Ser	Gln	
138			415					420					425				
140	agc	acc	agt	gtt	tca	act	aag	aaa	gaa	gat	gag	aca	atc	aca	agg	ccc	1407
141	Ser	Thr	Ser	Val	Ser	Thr	Lys	Lys	Glu	Asp	Glu	Thr	Ile	Thr	Arg	Pro	
142		430					435					440					
144	atc	ccc	tcg	gaa	gaa	aca	tcc	aca	gga	ata	aac	att	aca	acg	gtg	gct	1455
145	Ile	Pro	Ser	Glu	Glu	Thr	Ser	Thr	Gly	Ile	Asn	Ile	Thr	Thr	Val	Ala	
146	445				450					455						460	
148	att	cca	ttg	gtg	ctc	ctt	gtt	gtc	ctg	gtg	ttt	gct	gga	atg	ggg	atc	1503
149	Ile	Pro	Leu	Val	Leu	Val	Val	Leu	Val	Phe	Ala	Gly	Met	Gly	Ile		
150				465				470					475				
152	ttt	gca	gcc	ttt	aga	aag	aag	aag	aaa	gga	agt	ccg	tat	gga	tca		1551
153	Phe	Ala	Ala	Phe	Arg	Lys	Lys	Lys	Lys	Lys	Gly	Ser	Pro	Tyr	Gly	Ser	
154			480					485					490				
156	gca	gag	gct	cag	aaa	aca	gac	tgt	tgg	aag	cag	att	aaa	tat	ccc	ttt	1599
157	Ala	Glu	Ala	Gln	Lys	Thr	Asp	Cys	Trp	Lys	Gln	Ile	Lys	Tyr	Pro	Phe	
158		495					500				505						
160	gcc	aga	cat	cag	tca	gct	gag	ttt	acc	atc	agc	tat	gat	aat	gag	aag	1647
161	Ala	Arg	His	Gln	Ser	Ala	Glu	Phe	Thr	Ile	Ser	Tyr	Asp	Asn	Glu	Lys	
162		510					515				520						
164	gag	atg	aca	caa	aag	tta	gat	ctc	atc	aca	agt	gat	atg	gca	gat	tac	1695
165	Glu	Met	Thr	Gln	Lys	Leu	Asp	Leu	Ile	Thr	Ser	Asp	Met	Ala	Asp	Tyr	
166	525				530				535				540				
168	cag	cag	ccc	ctc	atg	att	ggc	acc	ggg	aca	gtc	acg	agg	aag	ggc	tcc	1743
169	Gln	Gln	Pro	Leu	Met	Ile	Gly	Thr	Gly	Thr	Val	Thr	Arg	Lys	Gly	Ser	
170			545					550					555				
172	acc	ttc	cgg	ccc	atg	gac	acg	gat	gcc	gag	gag	gca	ggg	gtg	agc	acc	1791
173	Thr	Phe	Arg	Pro	Met	Asp	Thr	Asp	Ala	Glu	Glu	Ala	Gly	Val	Ser	Thr	
174			560					565					570				
176	gat	gcc	ggc	ggc	cac	tat	gac	tgc	ccg	cag	cgg	gcc	ggc	cgc	cac	gag	1839
177	Asp	Ala	Gly	Gly	His	Tyr	Asp	Cys	Pro	Gln	Arg	Ala	Gly	Arg	His	Glu	
178		575					580					585					
180	tac	gcg	ctg	ccc	ctg	gcg	ccc	ccg	gag	ccc	gag	tac	gcc	acg	ccc	atc	1887
181	Tyr	Ala	Leu	Pro	Leu	Ala	Pro	Pro	Glu	Pro	Glu	Tyr	Ala	Thr	Pro	Ile	
182		590					595				600						
184	gtg	gag	cgg	cac	gtg	ctg	cgc	gcc	cac	acg	ttc	tct	gcg	cag	agc	ggc	1935
185	Val	Glu	Arg	His	Val	Leu	Arg	Ala	His	Thr	Phe	Ser	Ala	Gln	Ser	Gly	
186	605				610				615							620	
188	tac	cgc	gtc	cca	ggg	ccc	cag	ccc	ggc	cac	aaa	cac	tcc	ctc	tcc	tcg	1983
189	Tyr	Arg	Val	Pro	Gly	Pro	Gln	Pro	Gly	His	Lys	His	Ser	Leu	Ser	Ser	
190			625					630					635				
192	ggc	ggc	ttc	tcc	ccc	gta	gcg	ggt	gtg	ggc	gcc	cag	gac	gga	gac	tat	2031
193	Gly	Gly	Phe	Ser	Pro	Val	Ala	Gly	Val	Gly	Ala	Gln	Asp	Gly	Asp	Tyr	
194			640					645					650				
196	caa	agg	cca	cac	agc	gca	cag	cct	gcg	gac	agg	ggc	tac	gac	cgg	ccc	2079
197	Gln	Arg	Pro	His	Ser	Ala	Gln	Pro	Ala	Asp	Arg	Gly	Tyr	Asp	Arg	Pro	

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198          655          660          665
200 aaa gct gtc agc gcc ctc gcc acc gaa agc gga cac cct gac tct cag      2127
201 Lys Ala Val Ser Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln
202          670          675          680
204 aag ccc cca acg cat ccc ggg acg agt gac agc tat tct gcc ccc aga      2175
205 Lys Pro Pro Thr His Pro Gly Thr Ser Asp Ser Tyr Ser Ala Pro Arg
206 685          690          695          700
208 gac tgc ctc aca ccc ctc aac cag acg gcc atg act gcc ctt ttg tga      2223
209 Asp Cys Leu Thr Pro Leu Asn Gln Thr Ala Met Thr Ala Leu Leu *
210          705          710          715
212 acacaatgtg aaagaagcct gctgtggtac tgagcgtcgg gctgtcacaa ggcactggaa      2283
213 gaaggaggcc tgctggtcca gagtgtgcgt gtgtatcgaa ctgaaagcat ttttaacatt      2343
214 cttctcctgg aagaaatgaa ttacttgaag catgaaaagc acaccagggt ggttgtttat      2403
215 ttagcaatta tgactgtaga tttaaaaaca agcaaagaaa caacacctca gcagctgcc      2463
216 gtttccttag tctccacttc agagggggat gcgaagaggt cggcccagct cgggtgacca      2523
217 tgaagggtggc acaggaatta cagtgtgaat ggctgtgtca gatgttttcg tacctcagat      2583
218 taaaaatatt gctgaggtca gacgccacaa ttttcatgac tttcttcaga agtagcacat      2643
219 tttcgtgact tccgctgtcc tctgaaaaac aaagttatgtt ggaacatggt catgcaaaag      2703
220 tgattctgac caagtctaaa tcgagctttt ctactgacat gaaactgttg gaaactgatc      2763
221 tcattttata agaaatgatt ttcccctcaa ggaggcgtct gtaattccag aacagtccag      2823
222 acatcagctg tacctcatgc tcagtagttt ttatttgagt ttcttttggt agttaactat      2883
223 gggagattta acctcttttg ccaaagaggg aagtgtgtgt gtttttttaa tagaaaatat      2943
224 ggacaaaaaa tttttttccc tgaagaatgt attataacc tatttggtgt gttattacat      3003
225 cctgtgaaat gtatatatgt taaaataatg ggggtgctgg aaggatcatg cagactagct      3063
226 gctgggttagt gtggagggga agtggtttac tttgtagagt ttacatggtt ttatgcgcac      3123
227 actaattgta ataaactatg ccaaacca      3151
229 <210> SEQ ID NO: 2
230 <211> LENGTH: 715
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
234 <400> SEQUENCE: 2
235 Met Val Pro Gly Ala Arg Gly Gly Gly Ala Leu Ala Arg Ala Ala Gly
236 1          5          10          15
237 Arg Gly Leu Leu Ala Leu Leu Leu Ala Val Ser Ala Pro Leu Arg Leu
238          20          25          30
239 Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu Val Thr Tyr Gln
240          35          40          45
241 Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn
242          50          55          60
243 His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu
244 65          70          75          80
245 Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser
246          85          90          95
247 Asp Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr Gly Pro Tyr Cys
248          100          105          110
249 Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val
250          115          120          125
251 Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu
252          130          135          140

```

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```

253 Leu Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu
254 145 150 155 160
255 Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala
256 165 170 175
257 Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly
258 180 185 190
259 Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile
260 195 200 205
261 Ile Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly
262 210 215 220
263 Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp
264 225 230 235 240
265 Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser
266 245 250 255
267 Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
268 260 265 270
269 Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly
270 275 280 285
271 Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser
272 290 295 300
273 Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu
274 305 310 315 320
275 Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
276 325 330 335
277 Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn
278 340 345 350
279 Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val
280 355 360 365
281 Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile
282 370 375 380
283 Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His
284 385 390 395 400
285 Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln
286 405 410 415
287 Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val
288 420 425 430
289 Ser Thr Lys Lys Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu
290 435 440 445
291 Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val
292 450 455 460
293 Leu Leu Val Val Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe
294 465 470 475 480
295 Arg Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln
296 485 490 495
297 Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
298 500 505 510
300 Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
301 515 520 525
302 Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:925 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:1093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

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L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13